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FIG. 1

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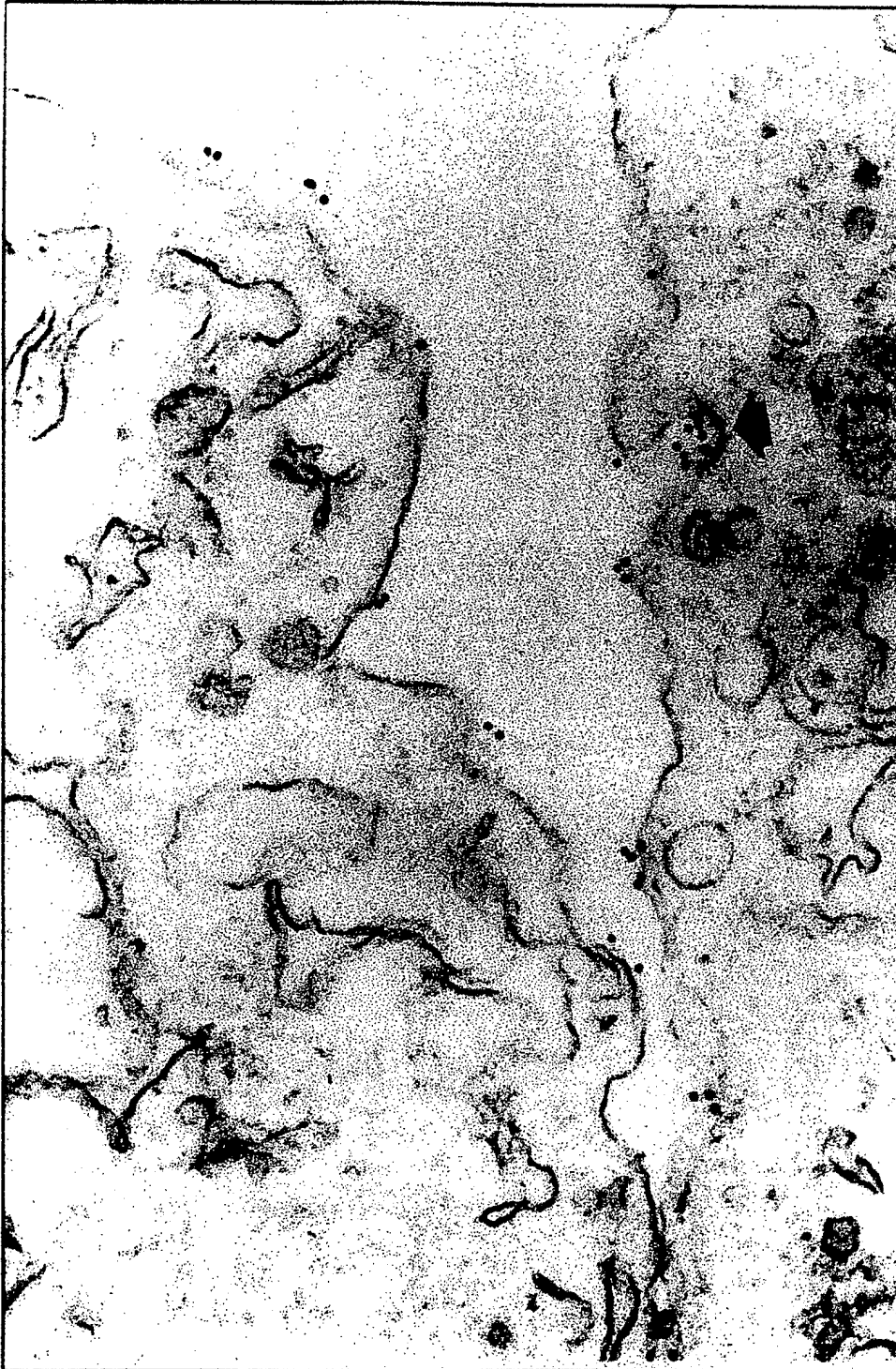


FIG. 2

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FIG. 3

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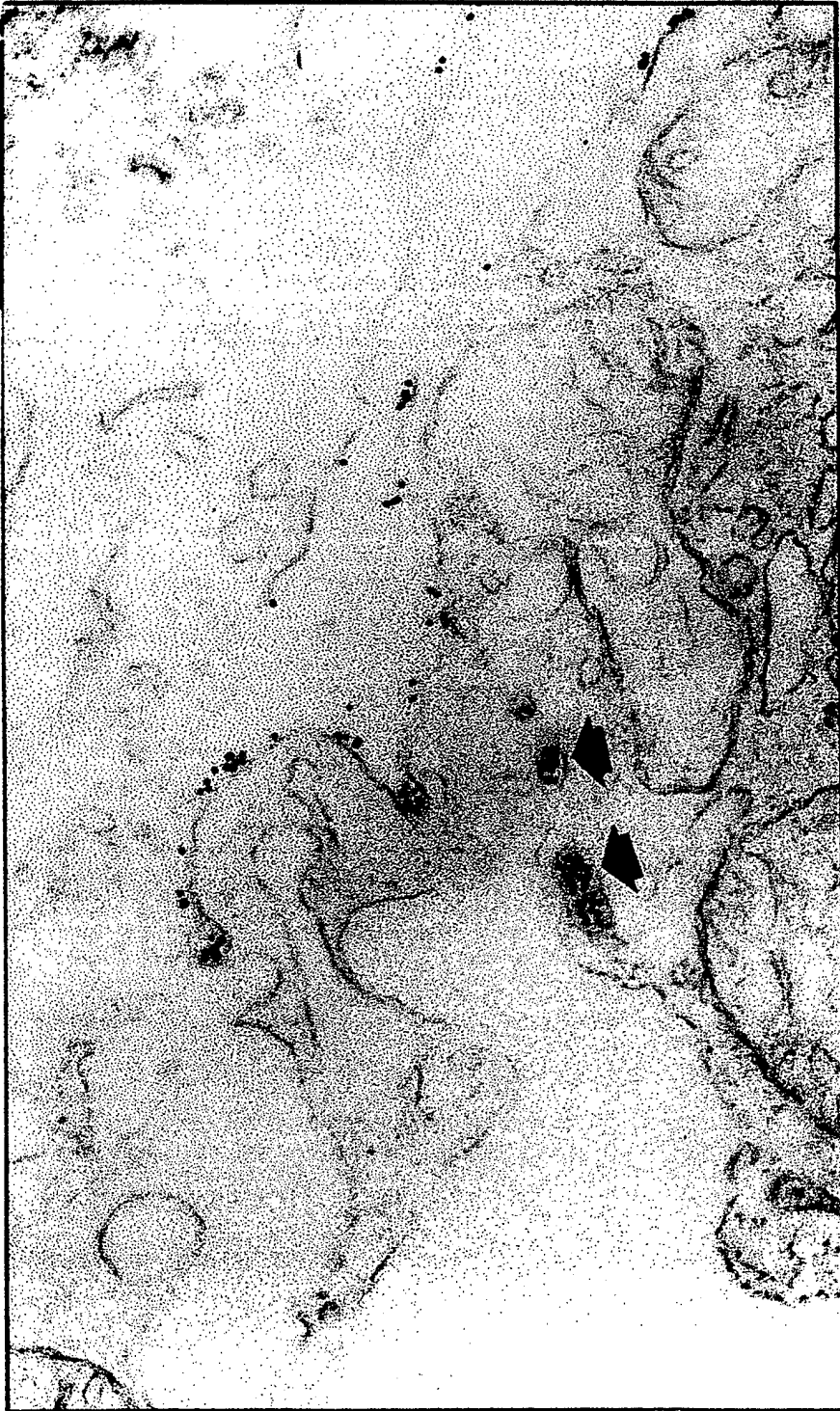


FIG. 4

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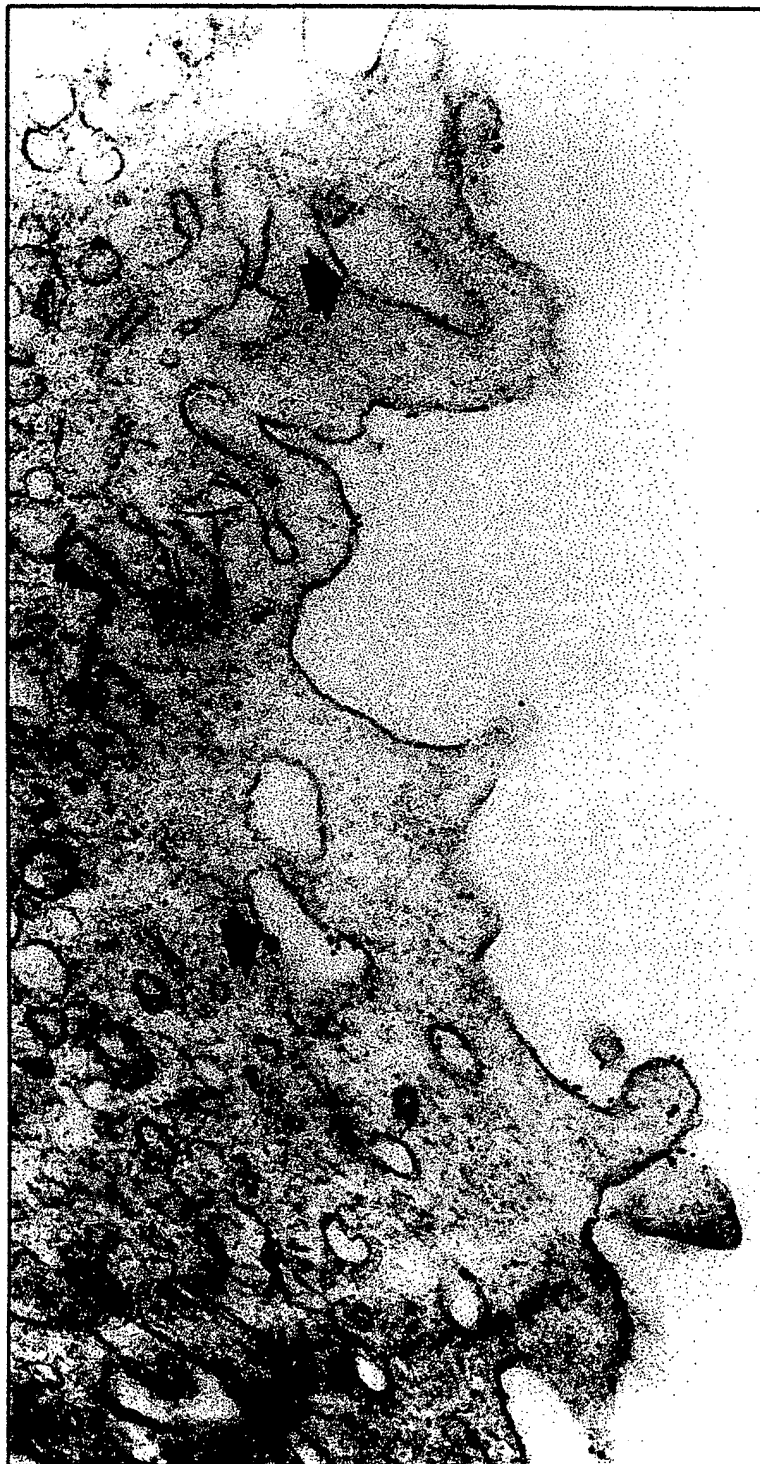


FIG. 5

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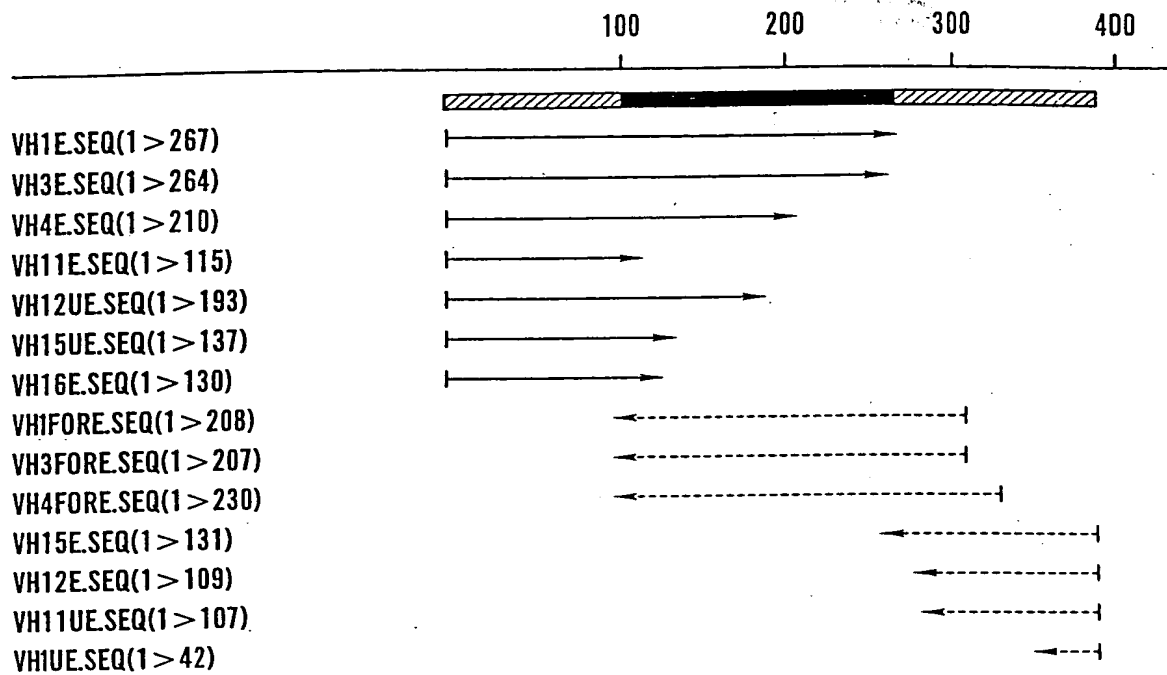


FIG. 6

ENZYMES: ALL 74 ENZYMES (NO FILTER)
SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

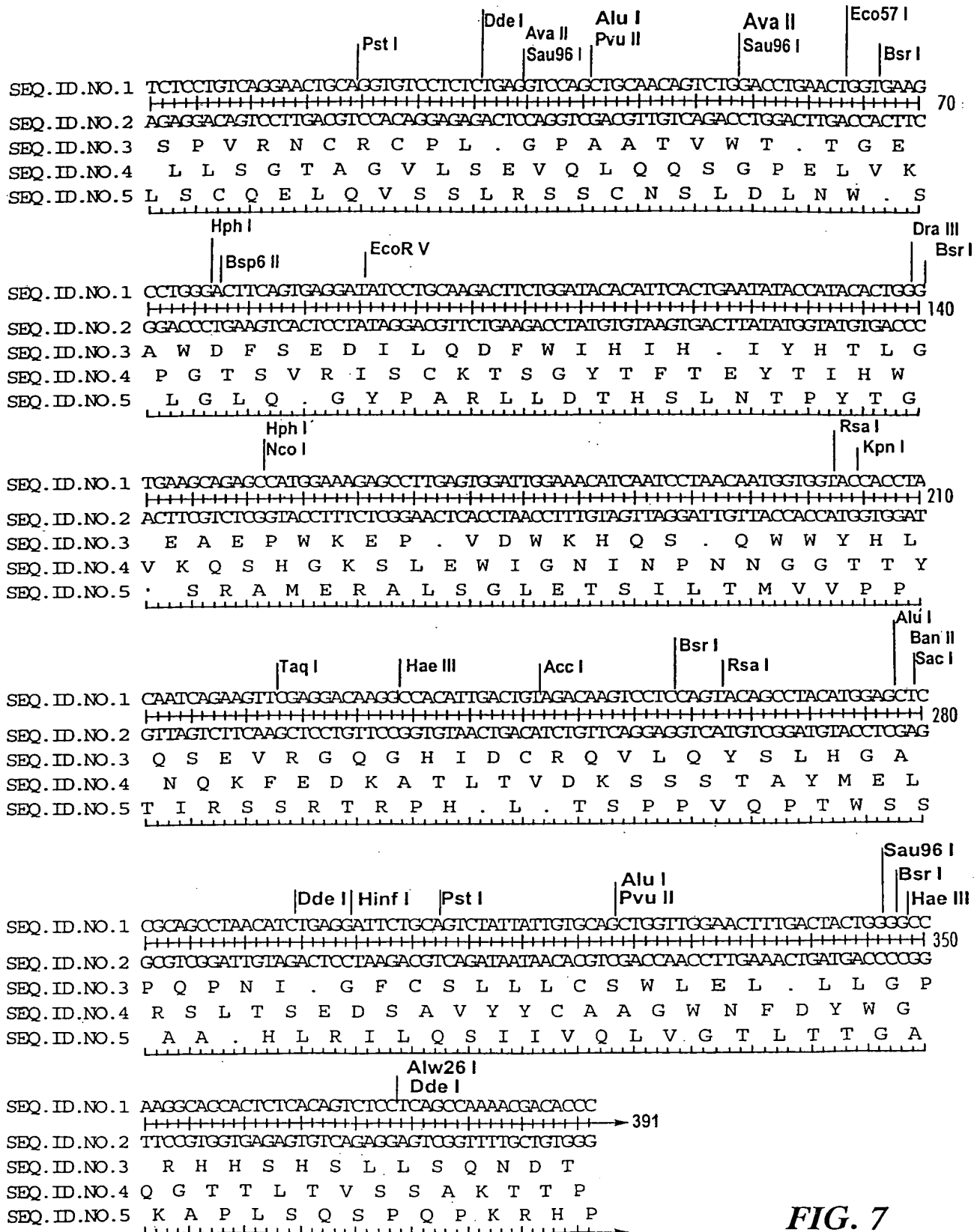


FIG. 7

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LIPMAN-PEARSON PROTEIN ALIGNMENT
 KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>115) J591VH.PRO	SEQ2(1>125) MUVHIIA.PRO	SIMILARITY INDEX	GAP NUMBER	GAP LENGTH	CONSENSUS LENGTH
(1>115)	(1>125)	75.6	2	10	125

```

      10      20      30      40      50
      ↓      ↓      ↓      ↓      ↓
EVQLQQSGPELVKPGTSVRISCKTSGYTFTEYTI-HWVKQSHGKSLEWIGNINPNNGGIT
EVQLQQSGPELVKPG:SV:ISCK:SGYTFT:Y : :WVKQS.GKSLEWIG:INP.NGGT:
EVQLQQSGPELVKPGASVKISCKASGYTFTDYMMNNWVKQSPGKSLEWIGDINPGNGGTS
      ↑      ↑      ↑      ↑      ↑      60
      10      20      30      40      50
      ↓      ↓      ↓      ↓      ↓
YNQKFEDKATLTVDKSSSTAYMELRSLTSEDSAVYYCAAG-----WNFDYWQGQGIT
YNQKF.:KATLTVDKSSSTAYM:L.SLTSEDSAVYYCA G ..FDYWQGQGIT
YNQKFKGKATLTVDKSSSTAYMQLSLTSEDSAVYYCARGYYSSSYMAYYAFDYWGQGIT
      ↑      ↑      ↑      ↑      ↑      120
      70      80      90      100     110

```

LTVSS
 :TVSS
 VIVSS

FIG. 8

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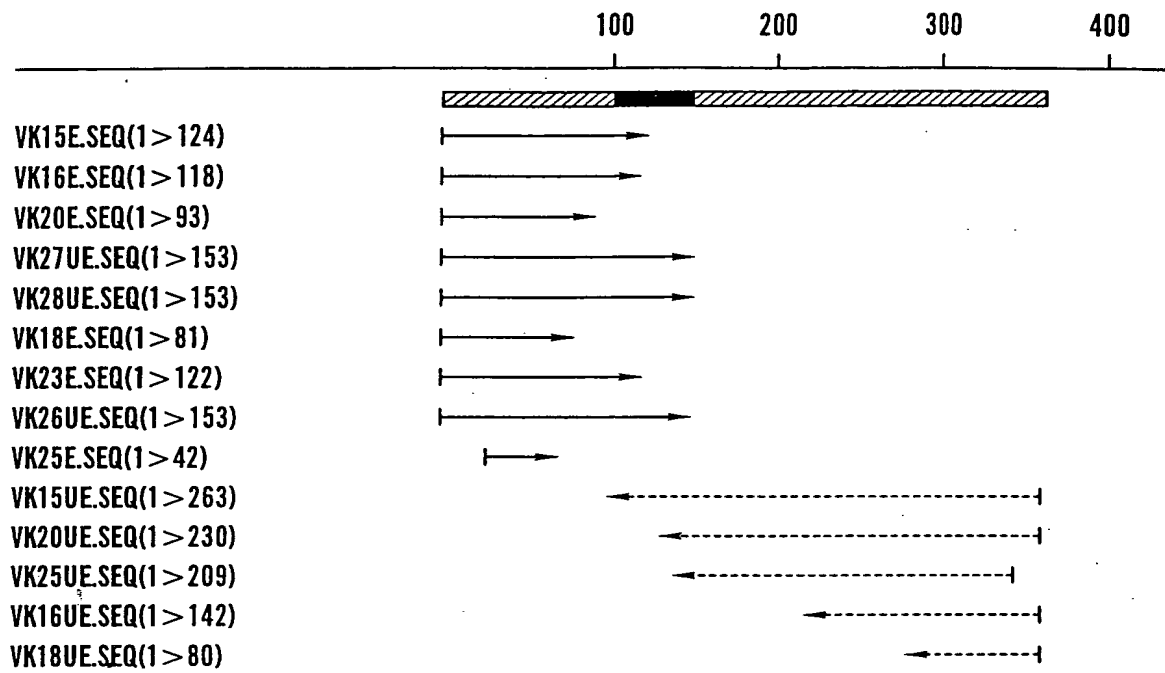


FIG. 9

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ENZYMES: ALL 74 ENZYMES (NO FILTER):
 SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

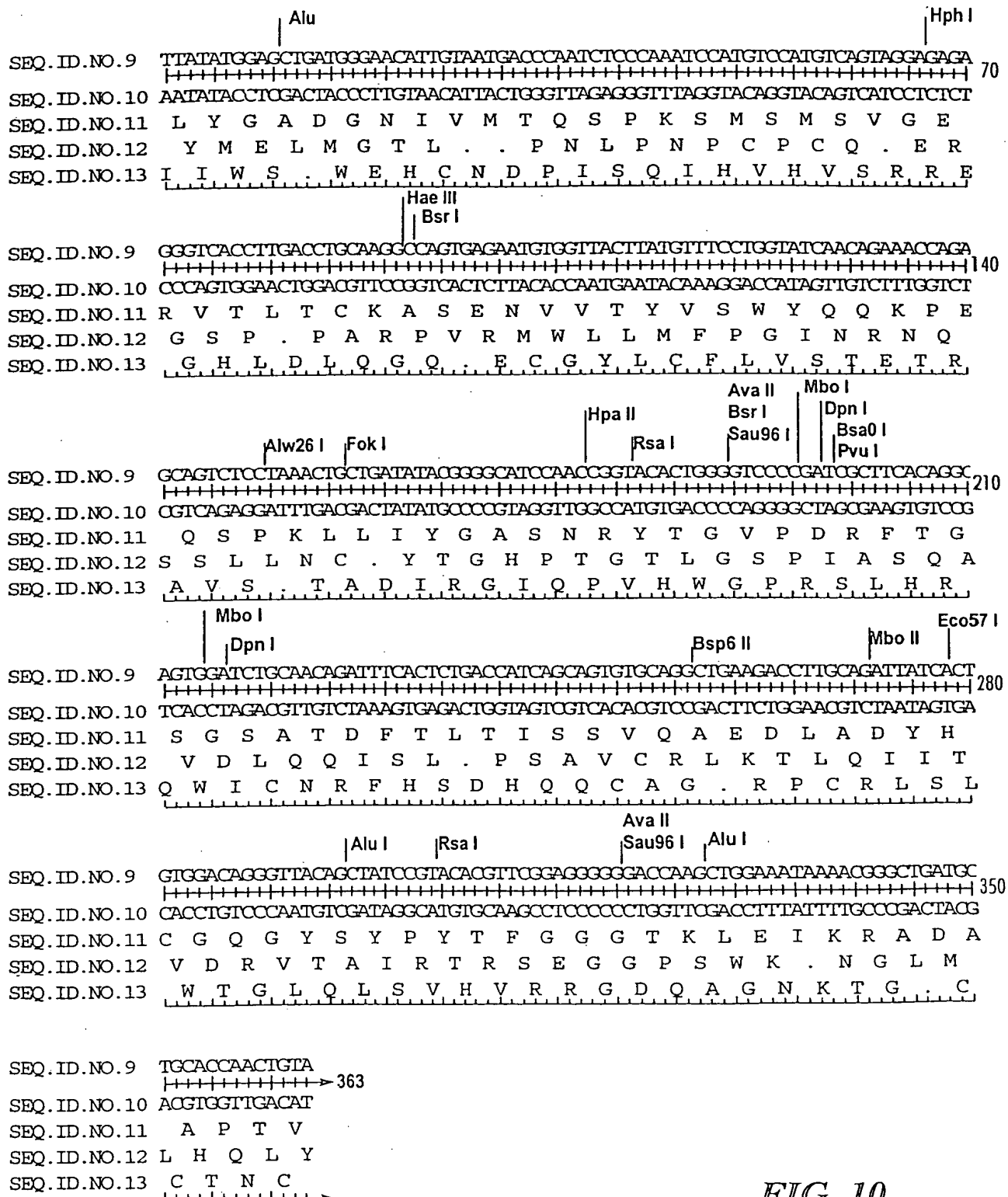


FIG. 10

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LIPMAN-PEARSON PROTEIN ALIGNMENT

KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>107)	SEQ2(1 > 1 1 1)	SIMILARITY	GAP	GAP	CONSENSUS
J591VK.PRO	MUVKV.PRO	INDEX	NUMBER	LENGTH	LENGTH
(1>107)	(1>109)	60.4	2	2	109

↓10 ↓20 ↓30 ↓40 ↓50
NIVMTQSPKSMMSVGERVILTCKAS-ENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVP
:I MIQSP.S:S S:G:RVT:TC:AS ::: .Y::WYQQKP. SPKLLIY AS. .:GVP
DIQMTQSPSSLSASLGDRVITTCRASQDDISNYLNWYQQKPGGSPKLLIYYASRLHSGVP
↑10 ↑20 ↑30 ↑40 ↑50 ↑60
↓60 ↓70 ↓80 ↓90 ↓100
DRFTGSGSATDFTLTISVQAEDLADYHCGQGYSY-PYTFGGGKLEIK
.RF:GSGS:TD::LTIS:::ED:A.Y C QG : P TFGGGKLEIK
SRFSGSGSGIDYSLTISNLEQEDIATYFCQQGNTLPRTTFGGGKLEIK
↑70 ↑80 ↑90 ↑100

FIG. 11